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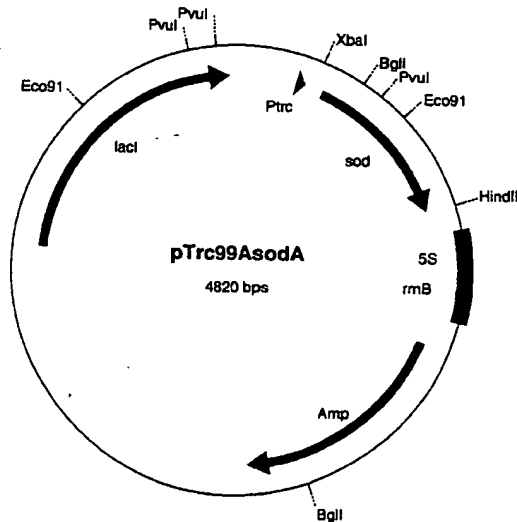
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(54) Title: PROCESS FOR THE PREPARATION OF L-AMINO ACIDS USING STRAINS OF THE ENTEROBACTERIACEAE FAMILY WHICH CONTAIN AN ENHANCED SODA GENE



(57) Abstract: The invention relates to a process for the preparation of L-amino acids, in particular L-threonine, in which the following steps are carried out: a) fermentation of microorganisms of the Enterobacteriaceae family which produce the desired L-amino acid and in which at least the sodA gene, or the nucleotide sequence which codes for this, is enhanced, in particular over-expressed, b) concentration of the desired L-amino acid in the medium or in the cells of the bacteria, and c) isolation of the desired L-amino acid.

**Process for the Preparation of L-Amino Acids using
Strains of the Enterobacteriaceae Family which Contain
an Enhanced sodA Gene**

Field of the Invention

- 5 This invention relates to a process for the fermentative preparation of L-amino acids, in particular L-threonine, using strains of the Enterobacteriaceae family in which at least the sodA gene is enhanced.

Prior Art

- 10 L-Amino acids, in particular L-threonine, are used in human medicine and in the pharmaceuticals industry, in the foodstuffs industry and very particularly in animal nutrition.

- It is known to prepare L-amino acids by fermentation of
15 strains of Enterobacteriaceae, in particular Escherichia coli (E. coli) and Serratia marcescens. Because of their great importance, work is constantly being undertaken to improve the preparation processes. Improvements to the process can relate to fermentation measures, such as e.g.
20 stirring and supply of oxygen, or the composition of the nutrient media, such as e.g. the sugar concentration during the fermentation, or the working up to the product form, by e.g. ion exchange chromatography, or the intrinsic output properties of the microorganism itself.

- 25 Methods of mutagenesis, selection and mutant selection are used to improve the output properties of these microorganisms. Strains which are resistant to antimetabolites, such as e.g. the threonine analogue α -amino- β -hydroxyvaleric acid (AHV), or are auxotrophic for
30 metabolites of regulatory importance and produce L-amino acid, such as e.g. L-threonine, are obtained in this manner.

Methods of the recombinant DNA technique have also been employed for some years for improving the strain of strains of the Enterobacteriaceae family which produce L-amino acids, by amplifying individual amino acid biosynthesis genes and investigating the effect on the production.

Object of the Invention

The object of the invention is to provide new measures for improved fermentative preparation of L-amino acids, in particular L-threonine.

Summary of the Invention

The invention provides a process for the fermentative preparation of L-amino acids, in particular L-threonine, using microorganisms of the Enterobacteriaceae family which in particular already produce L-amino acids and in which at least the nucleotide sequence which codes for the *sodA* gene is enhanced.

Detailed Description of the Invention

Where L-amino acids or amino acids are mentioned in the following, this means one or more amino acids, including their salts, chosen from the group consisting of L-asparagine, L-threonine, L-serine, L-glutamate, L-glycine, L-alanine, L-cysteine, L-valine, L-methionine, L-isoleucine, L-leucine, L-tyrosine, L-phenylalanine, L-histidine, L-lysine, L-tryptophan and L-arginine. L-Threonine is particularly preferred.

The term "enhancement" in this connection describes the increase in the intracellular activity of one or more enzymes or proteins in a microorganism which are coded by the corresponding DNA, for example by increasing the number of copies of the gene or genes, using a potent promoter or a gene or allele which codes for a corresponding enzyme or

protein with a high activity, and optionally combining these measures.

By enhancement measures, in particular over-expression, the activity or concentration of the corresponding protein is
5 in general increased by at least 10%, 25%, 50%, 75%, 100%, 150%, 200%, 300%, 400% or 500%, up to a maximum of 1000% or 2000%, based on that of the wild-type protein or the activity or concentration of the protein in the starting microorganism.

10 The process comprises carrying out the following steps:

- a) fermentation of microorganisms of the Enterobacteriaceae family in which at least the *sodA* gene is enhanced,
- 15 b) concentration of the corresponding L-amino acid in the medium or in the cells of the microorganisms of the Enterobacteriaceae family, and
- c) isolation of the desired L-amino acid, constituents of the fermentation broth and/or the biomass in its entirety or portions (> 0 to 100 %) thereof
20 optionally remaining in the product.

The microorganisms which the present invention provides can produce L-amino acids from glucose, sucrose, lactose, fructose, maltose, molasses, optionally starch, optionally cellulose or from glycerol and ethanol. They are
25 representatives of the Enterobacteriaceae family chosen from the genera *Escherichia*, *Erwinia*, *Providencia* and *Serratia*. The genera *Escherichia* and *Serratia* are preferred. Of the genus *Escherichia* the species *Escherichia coli* and of the genus *Serratia* the species *Serratia*
30 *marcescens* are to be mentioned in particular.

Suitable strains, which produce L-threonine in particular, of the genus *Escherichia*, in particular of the species *Escherichia coli*, are, for example

- Escherichia coli TF427
- 5 Escherichia coli H4578
- Escherichia coli KY10935
- Escherichia coli VNIIGenetika MG442
- Escherichia coli VNIIGenetika M1
- Escherichia coli VNIIGenetika 472T23
- 10 Escherichia coli BKIIM B-3996
- Escherichia coli kat 13
- Escherichia coli KCCM-10132.

Suitable L-threonine-producing strains of the genus *Serratia*, in particular of the species *Serratia marcescens*,
15 are, for example

- Serratia marcescens* HNr21
- Serratia marcescens* TLR156
- Serratia marcescens* T2000.

Strains from the Enterobacteriaceae family which produce L-
20 threonine preferably have, inter alia, one or more genetic or phenotypic features chosen from the group consisting of: resistance to α -amino- β -hydroxyvaleric acid, resistance to thialysine, resistance to ethionine, resistance to α -methylserine, resistance to diaminosuccinic acid,
25 resistance to α -aminobutyric acid, resistance to borrelidin, resistance to rifampicin, resistance to valine analogues, such as, for example, valine hydroxamate, resistance to purine analogues, such as, for example, 6-dimethylaminopurine, a need for L-methionine, optionally a
30 partial and compensatable need for L-isoleucine, a need for meso-diaminopimelic acid, auxotrophy in respect of threonine-containing dipeptides, resistance to L-threonine, resistance to L-methionine, resistance to L-glutamic acid,

resistance to L-aspartate, resistance to L-leucine,
resistance to L-phenylalanine, resistance to L-serine,
resistance to L-cysteine, resistance to L-valine,
sensitivity to fluoropyruvate, defective threonine
5 dehydrogenase, optionally an ability for sucrose
utilization, enhancement of the threonine operon,
enhancement of homoserine dehydrogenase I-aspartate kinase
I, preferably of the feed back resistant form, enhancement
of homoserine kinase, enhancement of threonine synthase,
10 enhancement of aspartate kinase, optionally of the feed
back resistant form, enhancement of aspartate semialdehyde
dehydrogenase, enhancement of phosphoenol pyruvate
carboxylase, optionally of the feed back resistant form,
enhancement of phosphoenol pyruvate synthase, enhancement
15 of transhydrogenase, enhancement of the RhtB gene product,
enhancement of the RhtC gene product, enhancement of the
YfiK gene product, enhancement of a pyruvate carboxylase,
and attenuation of acetic acid formation.

It has been found that microorganisms of the
20 Enterobacteriaceae family produce L-amino acids, in
particular L-threonine, in an improved manner after
enhancement, in particular over-expression, of the *sodA*
gene.

The nucleotide sequences of the genes of *Escherichia coli*
25 belong to the prior art and can also be found in the genome
sequence of *Escherichia coli* published by Blattner et al.
(*Science* 277: 1453-1462 (1997)).

The following information, inter alia, on the *sodA* gene is
known from the prior art:

30 Description: Superoxide dismutase
EC No. 1.15.1.1

- Reference: Touati; Journal of Bacteriology 155(3):
1078-1087 (1983); Schrum and Hassan; Free
Radical Biology and Medicine 17(3): 209-213
(1994); Benov and Fridovich; Archives of
5 Biochemistry and Biophysics 322(1): 291-294
(1995)

Accession No.: AE000465

The nucleic acid sequences can be found in the databanks of
the National Center for Biotechnology Information (NCBI) of
10 the National Library of Medicine (Bethesda, MD, USA), the
nucleotide sequence databank of the European Molecular
Biologies Laboratories (EMBL, Heidelberg, Germany or
Cambridge, UK) or the DNA databank of Japan (DDBJ, Mishima,
Japan).

- 15 The genes described in the text references mentioned can be
used according to the invention. Alleles of the genes which
result from the degeneracy of the genetic code or due to
"sense mutations" of neutral function can furthermore be
used.

- 20 To achieve an enhancement, for example, expression of the
genes or the catalytic properties of the proteins can be
increased. The two measures can optionally be combined.

To achieve an over-expression, the number of copies of the
corresponding genes can be increased, or the promoter and
25 regulation region or the ribosome binding site upstream of
the structural gene can be mutated. Expression cassettes
which are incorporated upstream of the structural gene act
in the same way. By inducible promoters, it is
additionally possible to increase the expression in the
30 course of fermentative L-threonine production. The
expression is likewise improved by measures to prolong the
life of the m-RNA. Furthermore, the enzyme activity is
also increased by providing the gene construct with a
protein. The genes or gene constructs can either be

present in plasmids with a varying number of copies, or can be integrated and amplified in the chromosome.

Alternatively, an over-expression of the genes in question can furthermore be achieved by changing the composition of
5 the media and the culture procedure.

Instructions in this context can be found by the expert, inter alia, in Chang and Cohen (Journal of Bacteriology 134: 1141-1156 (1978)), in Hartley and Gregori (Gene 13: 347-353 (1981)), in Amann and Brosius (Gene 40: 183-190
10 (1985)), in de Broer et al. (Proceedings of the National Academy of Sciences of the United States of America 80: 21-25 (1983)), in LaVallie et al. (BIO/TECHNOLOGY 11: 187-193 (1993)), in PCT/US97/13359, in Llosa et al. (Plasmid 26: 222-224 (1991)), in Quandt and Klipp (Gene 80: 161-169
15 (1989)), in Hamilton et al. (Journal of Bacteriology 171: 4617-4622 (1989)), in Jensen and Hammer (Biotechnology and Bioengineering 58: 191-195 (1998)) and in known textbooks of genetics and molecular biology.

Plasmid vectors which are capable of replication in
20 Enterobacteriaceae, such as e.g. cloning vectors derived from pACYC184 (Bartolomé et al.; Gene 102: 75-78 (1991)), pTrc99A (Amann et al.; Gene 69: 301-315 (1988)) or pSC101 derivatives (Vocke and Bastia; Proceedings of the National Academy of Sciences of the United States of America 80
25 (21): 6557-6561 (1983)) can be used. A strain transformed with a plasmid vector, where the plasmid vector carries at least the *sodA* gene, or the nucleotide sequence which codes for this, can be employed in a process according to the invention.

30 It is also possible to transfer mutations which affect the expression of the particular gene into various strains by sequence exchange (Hamilton et al.; Journal of Bacteriology 171: 4617-4622 (1989)), conjugation or transduction.

It may furthermore be advantageous for the production of L-amino acids, in particular L-threonine, with strains of the Enterobacteriaceae family, in addition to enhancement of the sodA gene, for one or more enzymes of the known
5 threonine biosynthesis pathway or enzymes of anaplerotic metabolism or enzymes for the production of reduced nicotinamide adenine dinucleotide phosphate or enzymes of glycolysis or PTS enzymes or enzymes of sulfur metabolism to be enhanced.

10 Thus, for example, at the same time one or more of the genes chosen from the group consisting of

- the thrABC operon which codes for aspartate kinase, homoserine dehydrogenase, homoserine kinase and threonine synthase (US-A-4,278,765),
- 15 • the pyc gene of Corynebacterium glutamicum which codes for pyruvate carboxylase (WO 99/18228),
- the pps gene which codes for phosphoenol pyruvate synthase (Molecular and General Genetics 231(2): 332-336 (1992)),
- 20 • the ppc gene which codes for phosphoenol pyruvate carboxylase (Gene 31: 279-283 (1984)),
- the pntA and pntB genes which code for transhydrogenase (European Journal of Biochemistry 158: 647-653 (1986)),
- the rhtB gene which imparts homoserine resistance (EP-A-
25 0 994 190),
- the mgo gene which codes for malate:quinone oxidoreductase (WO 02/06459),
- the rhtC gene which imparts threonine resistance (EP-A-1
013 765),

- the thrE gene of Corynebacterium glutamicum which codes for the threonine export protein (WO 01/92545),
- the gdhA gene which codes for glutamate dehydrogenase (Nucleic Acids Research 11: 5257-5266 (1983); Gene 23: 199-209 (1983)),
- the hns gene which codes for the DNA-binding protein HLP-II (Molecular and General Genetics 212: 199-202 (1988)),
- the pgm gene which codes for phosphoglucomutase (Journal of Bacteriology 176: 5847-5851 (1994)),
- the fba gene which codes for fructose biphosphate aldolase (Biochemical Journal 257: 529-534 (1989)),
- the ptsH gene of the ptsHIcrr operon which codes for the phosphohistidine protein hexose phosphotransferase of the phosphotransferase system PTS (Journal of Biological Chemistry 262: 16241-16253 (1987)),
- the ptsI gene of the ptsHIcrr operon which codes for enzyme I of the phosphotransferase system PTS (Journal of Biological Chemistry 262: 16241-16253 (1987)),
- the crr gene of the ptsHIcrr operon which codes for the glucose-specific IIA component of the phosphotransferase system PTS (Journal of Biological Chemistry 262: 16241-16253 (1987)),
- the ptsG gene which codes for the glucose-specific IIBC component (Journal of Biological Chemistry 261: 16398-16403 (1986)),
- the lrp gene which codes for the regulator of the leucine regulon (Journal of Biological Chemistry 266: 10768-10774 (1991)),

- the mopB gene which codes for 10 Kd chaperone (Journal of Biological Chemistry 261: 12414-12419 (1986)) and is also known by the name groES,
- the ahpC gene of the ahpCF operon which codes for the small sub-unit of alkyl hydroperoxide reductase (Proceedings of the National Academy of Sciences of the United States of America 92: 7617-7621 (1995)),
- the ahpF gene of the ahpCF operon which codes for the large sub-unit of alkyl hydroperoxide reductase (Proceedings of the National Academy of Sciences of the United States of America 92: 7617-7621 (1995)),
- the cysK gene which codes for cysteine synthase A (Journal of Bacteriology 170: 3150-3157 (1988)),
- the cysB gene which codes for the regulator of the cys regulon (Journal of Biological Chemistry 262: 5999-6005 (1987)),
- the cysJ gene of the cysJHIH operon which codes for the flavoprotein of NADPH sulfite reductase (Journal of Biological Chemistry 264: 15796-15808 (1989), Journal of Biological Chemistry 264: 15726-15737 (1989)),
- the cysI gene of the cysJHIH operon which codes for the haemoprotein of NADPH sulfite reductase (Journal of Biological Chemistry 264: 15796-15808 (1989), Journal of Biological Chemistry 264: 15726-15737 (1989)),
- the cysH gene of the cysJHIH operon which codes for adenylyl sulfate reductase (Journal of Biological Chemistry 264: 15796-15808 (1989), Journal of Biological Chemistry 264: 15726-15737 (1989)),
- the phoB gene of the phoBR operon which codes for the positive regulator PhoB of the pho regulon (Journal of Bacteriology 170: 3150-3157 (1988)),

- the *phoR* gene of the *phoBR* operon which codes for the sensor protein of the *pho* regulon (Journal of Molecular Biology 192 (3): 549-556 (1986)),
- the *phoE* gene which codes for protein E of the outer
5 cell membrane (Journal of Molecular Biology 163 (4): 513-532 (1983)),
- the *malE* gene which codes for the periplasmic binding protein of maltose transport (Journal of Biological Chemistry 259 (16): 10606-10613 (1984)),
- 10 • the *pykF* gene which codes for fructose-stimulated pyruvate kinase I (Journal of Bacteriology 177 (19): 5719-5722 (1995)),
- the *talB* gene which codes for transaldolase B (Journal of Bacteriology 177 (20): 5930-5936 (1995)),
- 15 • the *rseA* gene of the *rseABC* operon which codes for a membrane protein with anti- σ E activity (Molecular Microbiology 24 (2): 355-371 (1997)),
- the *rseC* gene of the *rseABC* operon which codes for a global regulator of the σ E factor (Molecular
20 Microbiology 24 (2): 355-371 (1997)),
- the *pfkB* gene which codes for 6-phosphofructokinase II (Gene 28 (3): 337-342 (1984)),
- the *sucA* gene of the *sucABCD* operon which codes for the decarboxylase sub-unit of 2-ketoglutarate dehydrogenase
25 (European Journal of Biochemistry 141 (2): 351-359 (1984)),
- the *sucB* gene of the *sucABCD* operon which codes for the dihydrolipoyltranssuccinase E2 sub-unit of 2-ketoglutarate dehydrogenase (European Journal of
30 Biochemistry 141 (2): 351-359 (1984)),

- the *sucC* gene of the *sucABCD* operon which codes for the β -sub-unit of succinyl-CoA synthetase (Biochemistry 24 (22): 6245-6252 (1985)) and
- the *sucD* gene of the *sucABCD* operon which codes for the
5 α -sub-unit of succinyl-CoA synthetase (Biochemistry 24 (22): 6245-6252 (1985)),

can be enhanced, in particular over-expressed.

It may furthermore be advantageous for the production of L-amino acids, in particular L-threonine, in addition to
10 enhancement of the *sodA* gene, for one or more of the genes chosen from the group consisting of

- the *tdh* gene which codes for threonine dehydrogenase (Journal of Bacteriology 169: 4716-4721 (1987)),
- the *mdh* gene which codes for malate dehydrogenase (E.C. 1.1.1.37) (Archives in Microbiology 149: 36-42 (1987)),
15
- the gene product of the open reading frame (orf) *yjfa* (Accession Number AAC77180 of the National Center for Biotechnology Information (NCBI, Bethesda, MD, USA)),
- the gene product of the open reading frame (orf) *ytff*
20 (Accession Number AAC77179 of the National Center for Biotechnology Information (NCBI, Bethesda, MD, USA)),
- the *pckA* gene which codes for the enzyme phosphoenolpyruvate carboxykinase (Journal of Bacteriology 172: 7151-7156 (1990)),
- 25 • the *poxB* gene which codes for pyruvate oxidase (Nucleic Acids Research 14(13): 5449-5460 (1986)),
- the *aceA* gene which codes for the enzyme isocitrate lyase (Journal of Bacteriology 170: 4528-4536 (1988)),

- the dgsA gene which codes for the DgsA regulator of the phosphotransferase system (Bioscience, Biotechnology and Biochemistry 59: 256-251 (1995)) and is also known under the name of the mlc gene,
- 5 • the fruR gene which codes for the fructose repressor (Molecular and General Genetics 226: 332-336 (1991)) and is also known under the name of the cra gene and
- the rpoS gene which codes for the sigma³⁸ factor (WO 01/05939) and is also known under the name of the katF
10 gene,

to be attenuated, in particular eliminated or for the expression thereof to be reduced.

The term "attenuation" in this connection describes the reduction or elimination of the intracellular activity of
15 one or more enzymes (proteins) in a microorganism which are coded by the corresponding DNA, for example by using a weak promoter or a gene or allele which codes for a corresponding enzyme with a low activity or inactivates the corresponding enzyme (protein) or gene, and optionally
20 combining these measures.

By attenuation measures, the activity or concentration of the corresponding protein is in general reduced to 0 to 75%, 0 to 50%, 0 to 25%, 0 to 10% or 0 to 5% of the activity or concentration of the wild-type protein or of
25 the activity or concentration of the protein in the starting microorganism.

It may furthermore be advantageous for the production of L-amino acids, in particular L-threonine, in addition to enhancement of the sodA gene, to eliminate undesirable side
30 reactions (Nakayama: "Breeding of Amino Acid Producing Microorganisms", in: Overproduction of Microbial Products, Krumphanzl, Sikyta, Vanek (eds.), Academic Press, London, UK, 1982).

The microorganisms produced according to the invention can be cultured in the batch process (batch culture), the fed batch process (feed process) or the repeated fed batch process (repetitive feed process). A summary of known
5 culture methods is described in the textbook by Chmiel (Bioprozesstechnik 1. Einführung in die Bioverfahrenstechnik [Bioprocess Technology 1. Introduction to Bioprocess Technology (Gustav Fischer Verlag, Stuttgart, 1991)) or in the textbook by Storhas (Bioreaktoren und
10 periphere Einrichtungen [Bioreactors and Peripheral Equipment] (Vieweg Verlag, Braunschweig/Wiesbaden, 1994)).

The culture medium to be used must meet the requirements of the particular strains in a suitable manner. Descriptions of culture media for various microorganisms are contained
15 in the handbook "Manual of Methods for General Bacteriology" of the American Society for Bacteriology (Washington D.C., USA, 1981).

Sugars and carbohydrates, such as e.g. glucose, sucrose, lactose, fructose, maltose, molasses, starch and optionally
20 cellulose, oils and fats, such as e.g. soya oil, sunflower oil, groundnut oil and coconut fat, fatty acids, such as e.g. palmitic acid, stearic acid and linoleic acid, alcohols, such as e.g. glycerol and ethanol, and organic acids, such as e.g. acetic acid, can be used as the source
25 of carbon. These substances can be used individually or as a mixture.

Organic nitrogen-containing compounds, such as peptones, yeast extract, meat extract, malt extract, corn steep liquor, soya bean flour and urea, or inorganic compounds,
30 such as ammonium sulfate, ammonium chloride, ammonium phosphate, ammonium carbonate and ammonium nitrate, can be used as the source of nitrogen. The sources of nitrogen can be used individually or as a mixture.

Phosphoric acid, potassium dihydrogen phosphate or dipotassium hydrogen phosphate or the corresponding sodium-containing salts can be used as the source of phosphorus. The culture medium must furthermore comprise salts of
5 metals, such as e.g. magnesium sulfate or iron sulfate, which are necessary for growth. Finally, essential growth substances, such as amino acids and vitamins, can be employed in addition to the abovementioned substances. Suitable precursors can moreover be added to the culture
10 medium. The starting substances mentioned can be added to the culture in the form of a single batch, or can be fed in during the culture in a suitable manner.

Basic compounds, such as sodium hydroxide, potassium hydroxide, ammonia or aqueous ammonia, or acid compounds,
15 such as phosphoric acid or sulfuric acid, can be employed in a suitable manner to control the pH of the culture. Antifoams, such as e.g. fatty acid polyglycol esters, can be employed to control the development of foam. Suitable substances having a selective action, e.g. antibiotics, can
20 be added to the medium to maintain the stability of plasmids. To maintain aerobic conditions, oxygen or oxygen-containing gas mixtures, such as e.g. air, are introduced into the culture. The temperature of the culture is usually 25°C to 45°C, and preferably 30°C to
25 40°C. Culturing is continued until a maximum of L-amino acids or L-threonine has formed. This target is usually reached within 10 hours to 160 hours.

The analysis of L-amino acids can be carried out by anion exchange chromatography with subsequent ninhydrin
30 derivation, as described by Spackman et al. (Analytical Chemistry 30: 1190-1206 (1958)), or it can take place by reversed phase HPLC as described by Lindroth et al. (Analytical Chemistry 51: 1167-1174 (1979)).

The process according to the invention is used for the
35 fermentative preparation of L-amino acids, such as, for

example, L-threonine, L-isoleucine, L-valine, L-methionine, L-homoserine and L-lysine, in particular L-threonine.

The present invention is explained in more detail in the following with the aid of embodiment examples.

- 5 The minimal (M9) and complete media (LB) for *Escherichia coli* used are described by J.H. Miller (A Short Course in Bacterial Genetics (1992), Cold Spring Harbor Laboratory Press). The isolation of plasmid DNA from *Escherichia coli* and all techniques of restriction, ligation, Klenow and
10 alkaline phosphatase treatment are carried out by the method of Sambrook et al. (Molecular Cloning - A Laboratory Manual (1989) Cold Spring Harbor Laboratory Press). Unless described otherwise, the transformation of *Escherichia coli* is carried out by the method of Chung et al. (Proceedings
15 of the National Academy of Sciences of the United States of America 86: 2172-2175 (1989)).

The incubation temperature for the preparation of strains and transformants is 37°C.

Example 1

- 20 Construction of the expression plasmid pTrc99AsodA

The *sodA* gene from *E. coli* K12 is amplified using the polymerase chain reaction (PCR) and synthetic oligonucleotides. Starting from the nucleotide sequence of the *sodA* gene in *E. coli* K12 MG1655 (Accession Number
25 AE000465, Blattner et al. (Science 277: 1453-1462 (1997))), PCR primers are synthesized (MWG Biotech, Ebersberg, Germany). The sequences of the primers are modified such that recognition sites for restriction enzymes are formed. The recognition sequence for *Xba*I is chosen for the *sodA*
30 primer and the recognition sequence for *Hind*III for the *sodA*2 primer, which are marked by underlining in the nucleotide sequence shown below.

sodA1: 5' - CGCGGCATCTAGAAATCTGACGCCCCGACAATAC - 3'
(SEQ ID No. 1)

sodA2: 5' - CGCCTCATTGAAGCTTGCGGCAAATG - 3'
(SEQ ID No. 2)

5 The chromosomal E. coli K12 MG1655 DNA employed for the PCR
is isolated according to the manufacturer's instructions
with "Qiagen Genomic-tips 100/G" (QIAGEN, Hilden, Germany).
A DNA fragment approx. 700 bp in size can be amplified with
the specific primers under standard PCR conditions (Innis
10 et al. (1990) PCR Protocols. A Guide to Methods and
Applications, Academic Press) with Pfu-DNA polymerase
(Promega Corporation, Madison, USA).

The PCR product is ligated according to the manufacturer's
instructions with the vector pCR-Blunt II-TOPO (Zero Blunt
15 TOPO PCR Cloning Kit, Invitrogen, Groningen, The
Netherlands) and transformed into the E. coli strain TOP10.
Selection of plasmid-carrying cells takes place on LB agar,
to which 50 µg/ml kanamycin are added. After isolation of
the plasmid DNA, the vector pCR-Blunt II-TOPO-sodA is
20 cleaved with the restriction enzymes HindIII and XbaI and,
after separation in 0.8% agarose gel, the sodA fragment is
isolated with the aid of the QIAquick Gel Extraction Kit
(QIAGEN, Hilden, Germany). The vector pTrc99A (Pharmacia
Biotech, Uppsala, Sweden) is cleaved with the enzymes
25 HindIII and XbaI and ligation is carried out with the sodA
fragment isolated.

The E. coli strain XL1-Blue MRF' (Stratagene, La Jolla,
USA) is transformed with the ligation batch and plasmid-
carrying cells are selected on LB agar, to which 50 µg/ml
30 ampicillin are added. Successful cloning can be
demonstrated after plasmid DNA isolation by control
cleavage with the enzymes BglI, Eco91I and PvuII. The
plasmid is called pTrc99AsodA (Figure 1).

Example 2Preparation of L-threonine with the strain
MG442/pTrc99AsodA

5 The L-threonine-producing E. coli strain MG442 is described
in the patent specification US-A- 4,278,765 and deposited
as CMIM B-1628 at the Russian National Collection for
Industrial Microorganisms (VKPM, Moscow, Russia).

The strain MG442 is transformed with the expression plasmid
pTrc99AsodA described in example 1 and with the vector
10 pTrc99A and plasmid-carrying cells are selected on LB agar
with 50 µg/ml ampicillin. The strains MG442/pTrc99AsodA and
MG442/pTrc99A are formed in this manner. Selected
individual colonies are then multiplied further on minimal
medium with the following composition: 3.5 g/l Na₂HPO₄*2H₂O,
15 1.5 g/l KH₂PO₄, 1 g/l NH₄Cl, 0.1 g/l MgSO₄*7H₂O, 2 g/l
glucose, 20 g/l agar, 50 mg/l ampicillin. The formation of
L-threonine is checked in batch cultures of 10 ml contained
in 100 ml conical flasks. For this, 10 ml of preculture
medium of the following composition: 2 g/l yeast extract,
20 10 g/l (NH₄)₂SO₄, 1 g/l KH₂PO₄, 0.5 g/l MgSO₄*7H₂O, 15 g/l
CaCO₃, 20 g/l glucose, 50 mg/l ampicillin are inoculated
and the batch is incubated for 16 hours at 37°C and 180 rpm
on an ESR incubator from Kühner AG (Birsfelden,
Switzerland).

25 250 µl portions of this preculture are transinoculated into
10 ml of production medium (25 g/l (NH₄)₂SO₄, 2 g/l KH₂PO₄,
1 g/l MgSO₄*7H₂O, 0.03 g/l FeSO₄*7H₂O, 0.018 g/l MnSO₄*1H₂O,
30 30 g/l CaCO₃, 20 g/l glucose, 50 mg/l ampicillin) and the
batch is incubated for 48 hours at 37°C. The formation of
L-threonine by the starting strain MG442 is investigated in
the same manner, but no addition of ampicillin to the
medium takes place. After the incubation the optical
density (OD) of the culture suspension is determined with

an LP2W photometer from Dr. Lange (Düsseldorf, Germany) at a measurement wavelength of 660 nm.

The concentration of L-threonine formed is then determined in the sterile-filtered culture supernatant with an amino acid analyzer from Eppendorf-BioTronik (Hamburg, Germany) by ion exchange chromatography and post-column reaction with ninhydrin detection.

The result of the experiment is shown in Table 1.

Table 1

Strain	OD (660 nm)	L-Threonine g/l
MG442	5.6	1.4
MG442/pTrc99A	3.8	1.3
MG442/pTrc99AsodA	3.9	2.3

10

Brief Description of the Figure:

Figure 1: Map of the plasmid pTrc99AsodA containing the sodA gene.

The length data are to be understood as approx. data. The abbreviations and designations used have the following meaning:

- Amp: Ampicillin resistance gene
- lacI: Gene for the repressor protein of the trc promoter
- 20 • Ptrc: trc promoter region, IPTG-inducible
- sodA: Coding region of the sodA gene

- 5S: 5S rRNA region
- rrnBT: rRNA terminator region

The abbreviations for the restriction enzymes have the following meaning

- 5 • BglI: Restriction endonuclease from *Bacillus globigii*
(ATCC 49760)
- Eco91I: Restriction endonuclease from *Escherichia coli*
RFL 91
- HindIII: Restriction endonuclease from *Haemophilus*
10 *influenzae*
- PvuII: Restriction endonuclease from *Proteus vulgaris*
(ATCC 13315)
- XbaI: Restriction endonuclease from *Xanthomonas*
campestris

What is claimed is:

1. A process for the preparation of L-amino acids, in particular L-threonine, which comprises carrying out the following steps:
 - 5 a) fermentation of microorganisms of the Enterobacteriaceae family which produce the desired L-amino acid and in which at least the *sodA* gene, or the nucleotide sequence which codes for this, is enhanced, in particular over-expressed,
 - 10 b) concentration of the desired L-amino acid in the medium or in the cells of the microorganisms, and
 - c) isolation of the desired L-amino acid, constituents of the fermentation broth and/or the biomass in its entirety or portions (> 0 to 100%) thereof
 - 15 optionally remaining in the product.
2. A process as claimed in claim 1, wherein microorganisms in which further genes of the biosynthesis pathway of the desired L-amino acid are additionally enhanced are employed.
- 20 3. A process as claimed in claim 1, wherein microorganisms in which the metabolic pathways which reduce the formation of the desired L-amino acid are at least partly eliminated are employed.
4. A process as claimed in claim 1, wherein the expression
25 of the polynucleotide which codes for the *sodA* gene is increased.
5. A process as claimed in claim 1, wherein the regulatory
and/or catalytic properties of the polypeptide
(protein) for which the polynucleotide *sodA* codes are
30 improved or increased.

6. A process as claimed in claim 1, wherein, for the preparation of L-amino acids, microorganisms of the Enterobacteriaceae family in which in addition at the same time one or more of the genes chosen from the group consisting of:
- 6.1 the thrABC operon which codes for aspartate kinase, homoserine dehydrogenase, homoserine kinase and threonine synthase,
 - 6.2 the pyc gene which codes for pyruvate carboxylase,
 - 6.3 the pps gene which codes for phosphoenol pyruvate synthase,
 - 6.4 the ppc gene which codes for phosphoenol pyruvate carboxylase,
 - 6.5 the pntA and pntB genes which code for transhydrogenase,
 - 6.6 the rhtB gene which imparts homoserine resistance,
 - 6.7 the mgo gene which codes for malate:quinone oxidoreductase,
 - 6.8 the rhtC gene which imparts threonine resistance,
 - 6.9 the thrE gene which codes for the threonine export protein,
 - 6.10 the gdhA gene which codes for glutamate dehydrogenase,
 - 6.11 the hns gene which codes for the DNA-binding protein HLP-II,

- 6.12 the pgm gene which codes for phosphoglucosmutase,
- 6.13 the fba gene which codes for fructose biphosphate aldolase,
- 5 6.14 the ptsH gene which codes for the phosphohistidine protein hexose phosphotransferase,
- 6.15 the ptsI gene which codes for enzyme I of the phosphotransferase system,
- 10 6.16 the crr gene which codes for the glucose-specific IIA component,
- 6.17 the ptsG gene which codes for the glucose-specific IIBC component,
- 6.18 the lrp gene which codes for the regulator of the leucine regulon,
- 15 6.19 the mopB gene which codes for 10 Kd chaperone,
- 6.20 the ahpC gene which codes for the small sub-unit of alkyl hydroperoxide reductase,
- 6.21 the ahpF gene which codes for the large sub-unit of alkyl hydroperoxide reductase,
- 20 6.22 the cysK gene which codes for cysteine synthase A,
- 6.23 the cysB gene which codes for the regulator of the cys regulon,
- 25 6.24 the cysJ gene which codes for the flavoprotein of NADPH sulfite reductase,
- 6.25 the cysI gene which codes for the haemoprotein of NADPH sulfite reductase,

- 6.26 the *cysH* gene which codes for adenylyl sulfate reductase,
- 6.27 the *phoB* gene which codes for the positive regulator *PhoB* of the *pho* regulon,
- 5 6.28 the *phoR* gene which codes for the sensor protein of the *pho* regulon,
- 6.29 the *phoE* gene which codes for protein E of outer cell membrane,
- 10 6.30 the *malE* gene which codes for the periplasmic binding protein of maltose transport
- 6.31 the *pykF* gene which codes for fructose-stimulated pyruvate kinase I,
- 6.32 the *talB* gene which codes for transaldolase B,
- 15 6.33 the *rseA* gene which codes for a membrane protein which acts as a negative regulator on *sigmaE* activity,
- 6.34 the *rseC* gene which codes for a global regulator of the *sigmaE* factor,
- 20 6.35 the *pfkB* gene which codes for 6-phosphofructokinase II,
- 6.36 the *sucA* gene which codes for the decarboxylase sub-unit of 2-ketoglutarate dehydrogenase,
- 6.37 the *sucB* gene which codes for the dihydrolipoyltranssuccinase E2 sub-unit of 2-ketoglutarate dehydrogenase,
- 25 6.38 the *sucC* gene which codes for the β -sub-unit of succinyl-CoA synthetase,

6.39 the sucD gene which codes for the α -sub-unit of succinyl-CoA synthetase,

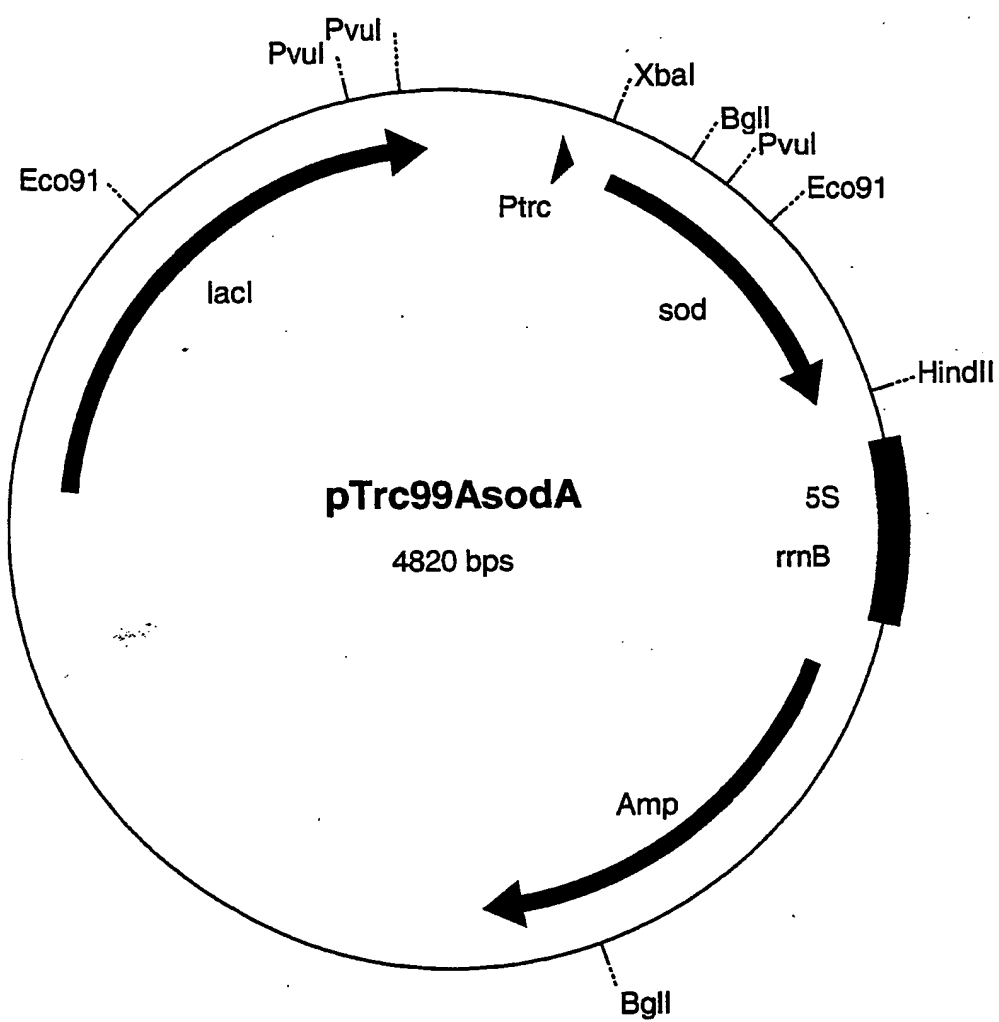
is or are enhanced, in particular over-expressed, are fermented.

5 7. A process as claimed in claim 1, wherein, for the preparation of L-amino acids, microorganisms of the Enterobacteriaceae family in which in addition at the same time one or more of the genes chosen from the group consisting of:

- 10 7.1 the tdh gene which codes for threonine dehydrogenase,
- 7.2 the mdh gene which codes for malate dehydrogenase,
- 15 7.3 the gene product of the open reading frame (orf) yjfA,
- 7.4 the gene product of the open reading frame (orf) ytfP,
- 7.5 the pckA gene which codes for phosphoenol pyruvate carboxykinase,
- 20 7.6 the poxB gene which codes for pyruvate oxidase,
- 7.7 the aceA gene which codes for isocitrate lyase,
- 7.8 the dgsA gene which codes for the DgsA regulator of the phosphotransferase system,
- 25 7.9 the fruR gene which codes for the fructose repressor,
- 7.10 the rpoS gene which codes for the sigma³⁸ factor

is or are attenuated, in particular eliminated or reduced in expression, are fermented.

Figure 1:



SEQUENCE PROTOCOL

5 <110> Degussa AG
 <120> Process for the preparation of L-amino acids using
 strains of the Enterobacteriaceae family which contain an
 enhanced sodA gene

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 <170> PatentIn version 3.1

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35 <220>
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 <223> sodA2

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45

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GM, HR, HU, ID, IL, IN, IS, JP, KE, KG, KP, KR, KZ, LC,
LK, LR, LS, LT, LU, LV, MA, MD, MG, MK, MN, MW,
MX, MZ, NO, NZ, OM, PH, PL, PT, RO, RU, SD, SE, SG,
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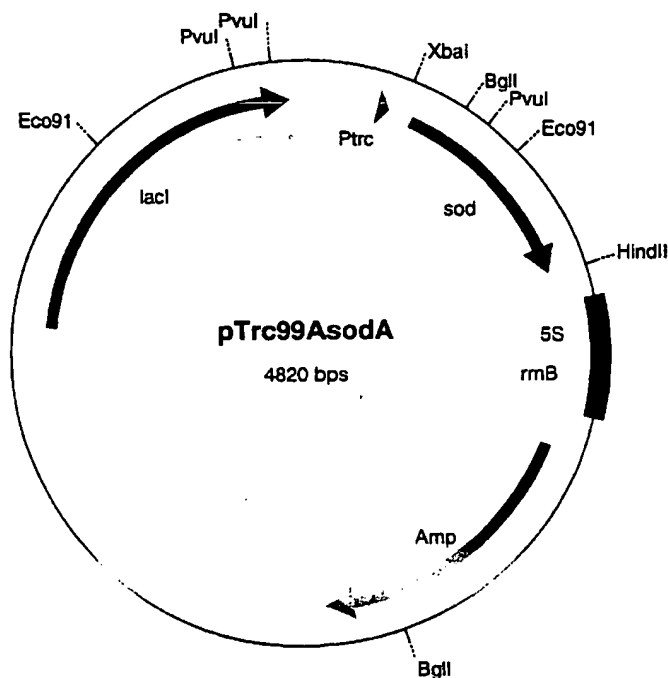
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(54) Title: PROCESS FOR THE PREPARATION OF L-AMINO ACIDS USING STRAINS OF THE ENTEROBACTERIACEAE FAMILY WHICH CONTAIN AN ENHANCED SODA GENE



(57) Abstract: The invention relates to a process for the preparation of L-amino acids, in particular L-threonine, in which the following steps are carried out: a) fermentation of microorganisms of the Enterobacteriaceae family which produce the desired L-amino acid and in which at least the sodA gene, or the nucleotide sequence which codes for this, is enhanced, in particular over-expressed, b) concentration of the desired L-amino acid in the medium or in the cells of the bacteria, and c) isolation of the desired L-amino acid.

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INTERNATIONAL SEARCH REPORT

International Application No
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A. CLASSIFICATION OF SUBJECT MATTER

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Minimum documentation searched (classification system followed by classification symbols)

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EPO-Internal, WPI Data, PAJ, BIOSIS, MEDLINE, FSTA, CHEM ABS Data

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INTERNATIONAL SEARCH REPORT

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C.(Continuation) DOCUMENTS CONSIDERED TO BE RELEVANT		
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A	<p>WO 98 04715 A (ARCHER DANIELS MIDLAND CO) 5 February 1998 (1998-02-05)</p>	
T	<p>WO 03 008600 A (DEGUSSA ;HERMANN THOMAS (DE)) 30 January 2003 (2003-01-30) claims 1-7</p>	1-7

INTERNATIONAL SEARCH REPORT

Information on patent family members

International Application No

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